SEQUENCE LISTING

<110> MINAMINO, NAOTO
KATAFUCHI, TAKESHI

<120> NOVEL PEPTIDES HAVING cAMP PRODUCING ACTIVITY

<130> 62273(71526)

<140> 10/516,768
<141> 2004-12-03

<150> PCT/JP03/06641
<151> 2003-05-28

<150> JP 2002-162797
<151> 2002-06-04

<160> 52

<170> PatentIn Ver. 3.3

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Gly Ser Pro Phe Asp Pro Ala Thr Leu Ser Glu Glu Glu Ser Arg Leu
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Leu Leu Ala Ala Met Val Asn Asp Tyr Glu Gln Met Lys Ala Arg Glu
50 55 60

Met Gln Lys Gln Arg Ala Gln Gly Ser Gly Ile Ser Val Gln Lys Arg
65 70 75 80

Ser Cys Asn Thr Ala Thr Cys Met Thr His Arg Leu Val Gly Leu Leu
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          30                  35                  40

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Glu Glu Ser Arg Leu Leu Leu Ala Ala Met Val Asn Asp Tyr Glu Gln
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Arg Leu Val Gly Leu Leu Ser Arg Ser Gly Ser Met Val Arg Ser Asn
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Asn Phe Trp Ile
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Asp Gly Arg Phe Asp Pro Ala Thr Leu Asp Glu Glu Glu Ser Arg Leu
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Leu Leu Ala Ala Met Val Asn Asp Tyr Glu Gln Met Arg Ala Arg Glu
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Ser Glu Lys Ala Gln Lys Thr Glu Gly Ser Arg Ile Gln Lys Arg Ala
65                  70                  75                  80

Cys Asn Thr Ala Thr Cys Met Thr His Arg Leu Ala Gly Trp Leu Ser
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20 25 30

Glu Asn Pro Pro Asp Ser Gly Val Arg Asn Glu Glu Glu Leu Arg Leu
35 40 45

Leu Leu Ala Ala Val Met Lys Asp Tyr Met Gln Met Lys Thr His Glu
50 55 60

Leu Glu Gln Glu Gln Glu Thr Glu Gly Ser Arg Val Ala Val Gln Lys
65 70 75 80

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Arg Ser Cys Asn Ser Ala Thr Cys Val Ala His Trp Leu Gly Gly Leu
                 85                  90                  95

Leu Ser Arg Ala Gly Ser Val Ala Asn Thr Asn Leu Leu Pro Thr Ser
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ttc tgg aaa ttt ccg ccc ttc ctg gtt ctc agc atc ctg gtc ctg tac      165
Phe Trp Lys Phe Pro Pro Phe Leu Val Leu Ser Ile Leu Val Leu Tyr
        5                  10                  15

cag gca ggc atg ttc cac aca gca ccc gtg aga ttg cct ttg gag agc      213
Gln Ala Gly Met Phe His Thr Ala Pro Val Arg Leu Pro Leu Glu Ser
    20                  25                  30

agc ttt gat tct gcc act ctc aca gag gag gaa gtg tcc ctt cta ctg      261
Ser Phe Asp Ser Ala Thr Leu Thr Glu Glu Glu Val Ser Leu Leu Leu
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Val Ala Met Val Lys Asp Tyr Val Gln Met Lys Ala Thr Val Leu Glu
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cag gag tca gag gac ttc agc atc act gcc cag gag aaa tcc tgc aac      357
Gln Glu Ser Glu Asp Phe Ser Ile Thr Ala Gln Glu Lys Ser Cys Asn
            70                  75                  80

act gct agc tgt gtg acc cac aag atg aca ggc tgg ctg agc aga tct      405
Thr Ala Ser Cys Val Thr His Lys Met Thr Gly Trp Leu Ser Arg Ser
        85                  90                  95

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    100                 105                 110

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Ile Leu Gly
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             20                  25                  30

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         35                  40                  45

Leu Leu Val Ala Met Val Lys Asp Tyr Val Gln Met Lys Ala Thr Val
     50                  55                  60

Leu Glu Gln Glu Ser Glu Asp Phe Ser Ile Thr Ala Gln Glu Lys Ser
 65                  70                  75                  80

Cys Asn Thr Ala Ser Cys Val Thr His Lys Met Thr Gly Trp Leu Ser
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Ser Lys Ile Leu Gly
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                        Met Gly Phe Trp Lys Phe Pro Pro Phe Leu
                        1               5                   10

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Val Leu Ser Ile Leu Val Leu Tyr Gln Ala Gly Met Phe His Thr Ala
                15                  20                  25

ccc gtg ag  gtaagacagc actggtggca gtgctctcgc ttcccacggc              5188
Pro Val Arg

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a ttg cct ttg gag agc agc ttt gat tct gcc act ctc aca gag gag gaa     5957
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gcc act gtg ctg gag cag gag tca gag gac ttc ag  gtcagtcttt          6050
Ala Thr Val Leu Glu Gln Glu Ser Glu Asp Phe Ser
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Ile Thr Ala Gln Glu Lys Ser Cys Asn Thr Ala Ser Cys Val Thr His
    75                  80                  85

aag atg aca ggc tgg ctg agc aga tct ggg agc gtg gct aag aac aac     6562
Lys Met Thr Gly Trp Leu Ser Arg Ser Gly Ser Val Ala Lys Asn Asn
90                  95                  100                 105

ttc atg ccc acc aat gtg gac tcc aaa atc ttg ggc tgacgccgca          6608
Phe Met Pro Thr Asn Val Asp Ser Lys Ile Leu Gly
                110                 115

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<213> Sus sp.

<220>
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Ser Arg Ser Gly Ser Val Val Lys Asn Asn Phe Met Pro Ile Asn Met
20 25 30

Gly Ser Lys Val Leu
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<210> 17
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<212> DNA
<213> Sus sp.

<220>
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<222> (112)..(486)

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Met Gly
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ttc tgg aag ttc ccc ccc ttc ctg atc ctc agc atc ctg gtc ctg tac 165
Phe Trp Lys Phe Pro Pro Phe Leu Ile Leu Ser Ile Leu Val Leu Tyr
5 10 15

caa gca gga atg ctc cat gcc gcg cca ttc agg atg gct ttg gga agc 213
Gln Ala Gly Met Leu His Ala Ala Pro Phe Arg Met Ala Leu Gly Ser
20 25 30

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agc ttt gat tct gcc aca ctc acg gaa gag gaa atg tcc ctc cta ctg      261
Ser Phe Asp Ser Ala Thr Leu Thr Glu Glu Glu Met Ser Leu Leu Leu
35                  40                  45                  50

gtt gca atg gtg aag gat tat gtg cag atg aag gcc act gtg ctg gag      309
Val Ala Met Val Lys Asp Tyr Val Gln Met Lys Ala Thr Val Leu Glu
                55                  60                  65

cag gag aca gag gac ttc agc atc acc acc cag gag aga tcc tgc aac      357
Gln Glu Thr Glu Asp Phe Ser Ile Thr Thr Gln Glu Arg Ser Cys Asn
            70                  75                  80

act gcc atc tgt gtg acc cac aag atg gca ggc tgg ctg agc aga tct      405
Thr Ala Ile Cys Val Thr His Lys Met Ala Gly Trp Leu Ser Arg Ser
        85                  90                  95

ggg agc gtg gtt aag aac aac ttc atg ccc atc aac atg ggc tcc aaa      453
Gly Ser Val Val Lys Asn Asn Phe Met Pro Ile Asn Met Gly Ser Lys
    100                 105                 110

gtc ttg ggc cgg cgc cgc aga cag cct cag gcc tgagctgtga aatgactcta    506
Val Leu Gly Arg Arg Arg Arg Gln Pro Gln Ala
115                 120                 125

aaaagaagtt gaactcaagt tgctttcact gcaaagttgc tttccctgca aattaaaaga    566

accaatttga aaaatagcat ggaagacaca catatatgca tgcttcttgc ttgaaataca    626

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<212> PRT
<213> Sus sp.

<400> 18

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Leu Tyr Gln Ala Gly Met Leu His Ala Ala Pro Phe Arg Met Ala Leu
             20                  25                  30

Gly Ser Ser Phe Asp Ser Ala Thr Leu Thr Glu Glu Glu Met Ser Leu
         35                  40                  45

Leu Leu Val Ala Met Val Lys Asp Tyr Val Gln Met Lys Ala Thr Val
     50                  55                  60

Leu Glu Gln Glu Thr Glu Asp Phe Ser Ile Thr Thr Gln Glu Arg Ser
 65                  70                  75                  80

Cys Asn Thr Ala Ile Cys Val Thr His Lys Met Ala Gly Trp Leu Ser
                 85                  90                  95

Arg Ser Gly Ser Val Val Lys Asn Asn Phe Met Pro Ile Asn Met Gly
            100                 105                 110
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Ser Lys Val Leu Gly Arg Arg Arg Arg Gln Pro Gln Ala
        115                 120                 125
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<210> 19
<211> 33
<212> PRT
<213> Sus sp.

<220>
<221> MOD_RES
<222> (1)
<223> pyroglutamic acid

<220>
<223> C-term amidated

<400> 19

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Glu Cys Asn Asn Leu Ser Thr Cys Val Leu Gly Thr Tyr Thr Trp Asp
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Val Asn Lys Phe Tyr Ala Phe Pro Leu Thr Thr Thr Gly Ile Arg Val
             20                  25                  30

Ser
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<210> 20
<211> 802
<212> DNA
<213> Sus sp.

<220>
<221> CDS
<222> (112)..(597)

<400> 20

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                                                          Met Gly
                                                          1

ttc tgg aag ttc ccc ccc ttc ctg atc ctc agc atc ctg gtc ctg tac      165
Phe Trp Lys Phe Pro Pro Phe Leu Ile Leu Ser Ile Leu Val Leu Tyr
        5                  10                  15

caa gca gga atg ctc cat gcc gcg cca ttc agg atg gct ttg gga agc      213
Gln Ala Gly Met Leu His Ala Ala Pro Phe Arg Met Ala Leu Gly Ser
    20                  25                  30

agc ttt gat tct gcc aca ctc acg gaa gag gaa atg tcc ctc cta ctg      261
Ser Phe Asp Ser Ala Thr Leu Thr Glu Glu Glu Met Ser Leu Leu Leu
35                  40                  45                  50
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gtt gca atg gtg aag gat tat gtg cag atg aag gcc act gtg ctg gag      309
Val Ala Met Val Lys Asp Tyr Val Gln Met Lys Ala Thr Val Leu Glu
                55                  60                  65

cag gag aca gag gac ttc agc ctg gac agc tcc aga gct aag cag tgc      357
Gln Glu Thr Glu Asp Phe Ser Leu Asp Ser Ser Arg Ala Lys Gln Cys
            70                  75                  80

aat aat ctg agt acc tgt gtg ctg gga aca tat aca tgg gac gtc aac      405
Asn Asn Leu Ser Thr Cys Val Leu Gly Thr Tyr Thr Trp Asp Val Asn
        85                  90                  95

aag ttt tat gca ttc ccc tta act aca act ggg att aga gta tct ggc      453
Lys Phe Tyr Ala Phe Pro Leu Thr Thr Thr Gly Ile Arg Val Ser Gly
    100                 105                 110

aag aaa tgg gtc agg gcc aga gtc tca gag aaa gtc cat tat ccc tca      501
Lys Lys Trp Val Arg Ala Arg Val Ser Glu Lys Val His Tyr Pro Ser
115                 120                 125                 130

agg cag cat acc cta agg tgc tta aga agg ccc cca ccc ctc ctc ctt      549
Arg Gln His Thr Leu Arg Cys Leu Arg Arg Pro Pro Pro Leu Leu Leu
                135                 140                 145

tct agt tcc tct cct aga att tgc atg tgt tct tct ctg gtt gct ctc      597
Ser Ser Ser Ser Pro Arg Ile Cys Met Cys Ser Ser Leu Val Ala Leu
            150                 155                 160

tgagctgcta tcagcagctt tccttgtggc catggatgtc tggaatatca gagaggaggt    657

gggggggtggg ggcaggcagg ccagaagaaa atcactcagg aatagattag gagagaatgg   717

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<210> 21
<211> 162
<212> PRT
<213> Sus sp.

<400> 21

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Met Gly Phe Trp Lys Phe Pro Pro Phe Leu Ile Leu Ser Ile Leu Val
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Leu Tyr Gln Ala Gly Met Leu His Ala Ala Pro Phe Arg Met Ala Leu
             20                  25                  30

Gly Ser Ser Phe Asp Ser Ala Thr Leu Thr Glu Glu Glu Met Ser Leu
         35                  40                  45

Leu Leu Val Ala Met Val Lys Asp Tyr Val Gln Met Lys Ala Thr Val
     50                  55                  60

Leu Glu Gln Glu Thr Glu Asp Phe Ser Leu Asp Ser Ser Arg Ala Lys
 65                  70                  75                  80
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Gln Cys Asn Asn Leu Ser Thr Cys Val Leu Gly Thr Tyr Thr Trp Asp
                 85                  90                  95

Val Asn Lys Phe Tyr Ala Phe Pro Leu Thr Thr Thr Gly Ile Arg Val
            100                 105                 110

Ser Gly Lys Lys Trp Val Arg Ala Arg Val Ser Glu Lys Val His Tyr
        115                 120                 125

Pro Ser Arg Gln His Thr Leu Arg Cys Leu Arg Arg Pro Pro Pro Leu
    130                 135                 140

Leu Leu Ser Ser Ser Ser Pro Arg Ile Cys Met Cys Ser Ser Leu Val
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Ala Leu
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<210> 22
<211> 7142
<212> DNA
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<400> 22

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Gly Ser Glu Ala Phe
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<220>
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Gly Ser Lys Ala Phe
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Gly Ser Asn Thr Tyr
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Pro Gln Gly Tyr
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Arg Phe Gly Thr Cys Thr Val Gln Lys Leu Ala His Gln Ile Tyr Gln
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Phe Thr Asp Lys Asp Lys Asp Gly Val Ala Pro Arg Ser Lys Ile Ser
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Pro Gln Gly Tyr
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Gly Phe Lys Val Phe
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